

METHOD OF DETERMINING THE THREE-DIMENSIONAL SHAPE OF A MACROMOLECULE

ABSTRACT OF THE DISCLOSURE

5 The present invention provides a fast and efficient method for determining the three-dimensional conformation of a protein. The steps of the method of the invention include: 1) formation of physical distance constraints, e.g., forming intramolecular chemical crosslinks of known size between residues of a protein; 2) enriching the number of the molecules that have intramolecular chemical crosslinks in the reaction pool, e.g., using size separation to remove
10 proteins with intermolecular bonds; 3) exposing the enriched reaction pool to a protease that cuts the protein at specific sites to produce peptide fragments; 4) measuring the size of the peptide fragments to determine linkage sites with a certain spatial relationship in the protein; and
5) interpreting the data produced to determine spatial geometry and protein structure based on the deduced spatial relationship of the linkage sites. The information is preferably analyzed with aid
15 from a computer system, which can be used to generate and/or analyze distance constraints between amino acids.